



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification<sup>6</sup>:C12N 15/31, C07K 14/22, 16/12, C12Q  
1/68, A61K 39/095, G01N 33/50

A2

(11) International Publication Number:

WO 99/57280

(43) International Publication Date:

11 November 1999 (11.11.99)

(21) International Application Number: PCT/US99/09346

(22) International Filing Date: 30 April 1999 (30.04.99)

## (30) Priority Data:

60/083,758	1 May 1998 (01.05.98)	US
60/094,869	31 July 1998 (31.07.98)	US
60/098,994	2 September 1998 (02.09.98)	US
60/099,062	2 September 1998 (02.09.98)	US
60/103,749	9 October 1998 (09.10.98)	US
60/103,794	9 October 1998 (09.10.98)	US
60/103,796	9 October 1998 (09.10.98)	US
60/121,528	25 February 1999 (25.02.99)	US

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(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

## Published

Without international search report and to be republished upon receipt of that report.

(54) Title: NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

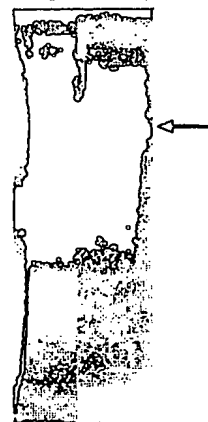
## (57) Abstract

The invention provides proteins from Neisseria meningitidis, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.

919 (46 kDa)

## A) PURIFICATION

M1 919



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EE	Estonia						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

a147.seq

```

1   ATGCGACGAG AAGCCAAAAT GGCACAAACT ACACTCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CTCCCAAGCG CATGGAAGTG
101 AGCAATCAGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCGG
151 CGCGCCACTT CGGGGCTGCT GCACACTTCT ACCGCCTCCG ACAAATCAT
201 CAGCGGCGAC ACCTTGCGAC AAAAAGCCGT CAACTTGGGT GATGCTTTAG
251 ACGGCGTACC GGGCATTCTT GCCTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC AGGCAGACGG ATTAAAGTGT TGAACCATCA
351 CGGCGAAACG GCGGACATGG CCGACTTCTC TCCAGACCAT GCAATCATGG
401 TGGACAGCGC CTTGTCGCAA CAGGTCGAAA TCCTGCGCGG TCCGGTTACG
451 CTCTTGTACA GCTCGGGCAA TGTGGCGGGG CTGGTTCGATG TTGCGGATGG
501 CAAAATCCCC GAAAAAATGC CTGAAAACGG CGTATCGGGC GAACTCGGAT
551 TGCCTTTGAG CAGCGGCAAT CTGGA AAAAC TCACGTCCGG CGGCATCAAT
601 ATCGGTTTGG GCAAAAACTT TGTATTGCAC ACGGAAGGGC TGTACCGCAA
651 ATCGGGGGAT TACGCCGTAC CGGTTTACCG CAATCTGAAA CGCCTGCCCG
701 ACAGCCACGC CGATTTCGCA ACGGGCAGCA TCGGGCTGTC TTGGGTTGGC
751 GAAAAAGGCT TTATCGGCGC AGCATAACAG GACCGTCGCG ACCAATATGG
801 TCTGCCTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGCAAAAGAG TTTGATTAAAC AAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAAT CCGGGCTTGA GCTGCGGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAACGGC AAACCTTGGA
1001 TAGACCTGCG CAACAAACGC TACGAACTCC GCGCCGAATG GAAGCAACCG
1051 TTCCCGGTTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGCG ATGCAGTAGA AAACCTTTTTT AACCAACAAA
1151 CGCAAAACGC CCGTATCGAG TTGCGCCACC AACCCATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCAATA TTTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCAGTGCT GCTTGACAAT AAAGTGCAAC
1301 ATTACAGCTT TTTCGGTGTA GAACAGGCAA ACTGGGACAA CTTACAGCTT
1351 GAAGGCGGCG TACGCGTGGA AAAACAAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGGAAA ACTACTACAA CCATCCCCTG CCCGACCTCG
1451 GCGCGCACCG CCAAACCGCC CGCTCATTCG CACTTTCGGG CAACCTTGAT
1501 TTCACGCCAC AACACAAACT CAGCCTGACC GCCTCCCATC AGGAACGCCT
1551 GCCGTCAACG CAAGAGCTGT ACGCACACGG CAAACACGTC GCCACCAACA
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGCGC TGGGCTACGA AGGCGACCGC TGGCAATACA ATCTGGCACT
1701 CTACCGCAAC CGCTTCGGCA ACTACATTTA CGCCCAAACC TTAAGACGAC
1751 GACGCGGCCC CAAATCCATC GAAGACGACA GCGAAATGAA GCTCGTGCGC
1801 TACAACCAAT CCGGTGCGGA CTTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACCGACA CCGCGCTACC GCATCGGCGT TTCCGCGGAC TATGTACGAG
1901 GCCGTCTGAA AAACCTGCCT TCCCTACCCG GCAGGGAAGA CGCCTACGGC
1951 AACC GCCCAC TCATTGCCA AGCCGACCAA AACGCCCTC GCGTTCGGC
2001 TGC GCGCCTC GCGTCCACC TGAAAGCCTC GCTGACCGAC CGCATCGATG
2051 CCAATTTGGA CTA TACCGC GTGTTGCGCC AAAACAAACT CGCCCGCTAC
2101 GAAACGCGCA CGCCCGGACA CCATATGCTC AACCTCGGCG CAAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGGAATTG GTACGTCAA GCGGACAACC
2201 TGCTCAACCA ATCCGTTTAC GCCCACAGCA GCTTCCTCTC TGATACGCCG
2251 CAAATGGGCC GCAGCTTTAC CGGCGGCGTG AACGTGAAGT TTAA

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This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

a147.pep

```

1   MRREAKMAQT TLKPIVLSIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFS PDH AIMVDSALSQ QVEILRGPVT
151 LLYSSGNVAG LVDVADGKIP EKMPENGVS G ELGLRLSSGN LEKLTSGGIN
201 IGLGKNFVLH TEGLYRKSGD YAVPRYRNLK RLPDSHADSQ TGSIGLSWVG
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
301 LTEEDIDYDN PGLSCGFHDD DDAHAHAHNG KPWIDLNRKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHDE KAGDAVENFF NNQTQNARIE LRHQPIGRLK
401 GSWG VQYLGQ KSSALSATSE AVKQPM LLDN KVQHYSFFGV EQANWDNFTL
451 EGGVRVEKQK ASIRYDKALI DRENYNHNPL PDLGAHRQTA RSFALSGNWX
501 FTPQHKLST ASHQERLPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGP KSI EDDSEMKLVR

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1101 AGGTCGTCTG AAAGGCAGCT GGGGCGTGCA ATATTTACAA CAAAAATCCA
1151 GTGCTTTATC TGCCATATCC GAAGCGGTTA AACAAACGAT GCTGCTTGAC
1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA
1251 CAACTTCACG CTTGAAGGAG GCGTACGCGT GGAAAAACAA AAAGCCTCCA
1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC
1351 CTGCCCGACC TCGGCGCGCA CCGCCAAACC GCCCGCTCAT TCGCACTTTC
1401 GGGCAACTGG TATTTACAGC CACAACACAA ACTCAGCCTG ACCGCTCCC
1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAAACAC
1501 GTCGCCACCA ACACCTTTGA AGTCGGCAAC AAACACCTCA ACAAAGAGCG
1551 TTCCAACAAT ATCGAACTCG CGCTGGGCTA CGAAGGCGAC CGCTGGCAAT
1601 ACAATCTGGC ACTCTACCGC AACCGCTTCG GTAACACAT TTACGCCCAA
1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT
1701 GAAGCTCGTG CGCTACAACC AATCCGGCGC CGACTTCTAC GGC CGGAAG
1751 GCGAAATCTA CTTCAAACCG ACACCGCGCT ACCGCATCGG CGTTTCCGGC
1801 GACTATGTAC GAGGCGGTCT GAAAAACCTG CCTTCCCTAC CCGGCAGAGA
1851 AGATGCCTAC GGCAACCGTC CTTTCATCGC ACAGGACGAC CAAAATGCCC
1901 CCCGTGTTCC GGCTGCGCGC CTCGGCTTCC ACCTGAAAGC CTCGCTGACC
1951 GACCGTATCG ATGCCAATTG GACTACTAC CGCGTGTTTC CCCAAACAA
2001 ACTCGCCCGC TACGAAACGC GCACGCCCGG ACACCATATG CTCAACCTCG
2051 GCGCAAATA CCGCCGCAAT ACGCGCTATG GCGAGTGGAA TTGGTACGTC
2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCACA GCAGCTTCT
2151 CTCTGATACG CCGCAAATGG GCCGCAGCTT TACCGCGCGC GTGAACGTGA
2201 AGTTTAA

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This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

```

m147.pep (partial)
1 ..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STASDKIISG DTLRQKAVNL
51 GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMAFSPD
101 HAIMVDTALS QQVEILRGPV TLLYSSGNVA GLVDVADGKI PEKMPENGVS
151 GELGLRLSSG NLEKLTSGLI NIGLGKNFVL HTEGLYRKSG DYAVPRYRNL
201 KRLPDSHADS QTGSIGLSWV GEKGFIGVAY SDRRDQYGLP AHSHEYDDCH
251 ADIIWOKSLI NKRYLQLYPH LLTEEDIDYD NPGLSCGFHD DDNAHAHTHS
301 GRPWIDLRNK RYELRAEWKQ PFPGFALRV HLNRRNDYRHD EKAGDAVENF
351 FNNQTQNARI ELRHQPIGRL KGSWGVQYLO QKSSALS AIS EAVKQPMLLD
401 NKVQHYSEFFG VEQANWDNFT LEGGVRVEKQ KASIYDKAL IDRENNYHNP
451 LPDLGAHRQT ARSFALSGNW YFTPOHKLST TASHQERLPS TQELYAHGKH
501 VATNTFEVGN KHLNKRSEN IELALGYEGD RWQYNLALYR NRGNYIYAG
551 TLNDGRGPKS IEDDSEMKLV RYNQSGADFY GAEGEIFYKP TPRYRIGVSG
601 DYVRGRLKNL PSLPGREDAY GNRPFIAQDD QNAPRVPAAR LGFHLKASLT
651 DRIDANLDYY RVFAQNKLAR YETRTPGHHM LNLGANYRRN TRYGEWNWYV
701 KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m147 / g147 92.3% identity in 142 aa overlap

```

                                10      20      30
m147.pep                      PHKTEQSVDL ETVSVVGKSR PRATSGLLHTS
                                | : | | | | | | | | | | | | | | | | | | | |
g147      MRREAKMAQITLKP I VLSILLINTPLLAQA HETE QSVGLETVSVVGKSR PRATSGLLHTS
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m147.pep      TASDKIISG DTLRQKAVNLGDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g147      TASDKIISG DTLRQKAVNLGDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
              70      80      90      100     110     120

                                100     110     120     130     140     150
m147.pep      GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGLVDVADGKI PEKMPENGVS
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g147      GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGAGQCCRWNPPKNA

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601 YNQSGADFYG AEGEIYFKPT PRYRIGVSGD YVRGRLKNLP SLPGREDAYG  
651 NRPLIAQADQ NAPRVPAARL GVHLKASLTD RIDANLDYR VFAQNKLARY  
701 ETRTPGHHML NLGANYRRNT RYGEWNWYVK ADNLLNQSVY AHSSFLSDTP  
751 QMGRSFTGGV NVKF\*

m147/a147 98.1% identity in 734 aa overlap

m147.pep				10	20	30
				PHKTEQSV	DLTVSVVGKSR	PRATSGLLHTS
a147	MRREAKMAQTTLKPIVLSILLINTPLLSQA	HGTEQSVG	LETVSVVGKSR	PRATSGLLHTS		
	10	20	30	40	50	60
m147.pep	40	50	60	70	80	90
	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGET				
a147	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGET				
	70	80	90	100	110	120
m147.pep	100	110	120	130	140	150
	GDMADFS	PDHAIMVDTALSQQVEILRGPVTL	LYSSGNVAGLVDVADGKIPEKMPENGVS			
a147	GDMADFS	PDHAIMVDSALSQQVEILRGPVTL	LYSSGNVAGLVDVADGKIPEKMPENGVS			
	130	140	150	160	170	180
m147.pep	160	170	180	190	200	210
	ELGLRLSSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNKRLPDSHADSQ				
a147	ELGLRLSSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNKRLPDSHADSQ				
	190	200	210	220	230	240
m147.pep	220	230	240	250	260	270
	TGSIGLSWVG	EKGFIGVAYS	DRRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHL		
a147	TGSIGLSWVG	EKGFIGAAYS	DRRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHL		
	250	260	270	280	290	300
m147.pep	280	290	300	310	320	330
	LTEEDIDYDNPGLSCGFHDD	NAHAHNSGRPWIDLRNKRYELRAEWKQFPFGFEALRVH				
a147	LTEEDIDYDNPGLSCGFHDD	DAHAHNGKPWIDLRNKRYELRAEWKQFPFGFEALRVH				
	310	320	330	340	350	360
m147.pep	340	350	360	370	380	390
	LNRNDYRHDEKAGDAVENFF	NQTNARIELRHQPIGRLKGSWGVQYLQKSSALSATSE				
a147	LNRNDYRHDEKAGDAVENFF	NQTNARIELRHQPIGRLKGSWGVQYLQKSSALSATSE				
	370	380	390	400	410	420
m147.pep	400	410	420	430	440	450
	AVKQPMLLDNKVQHYSFFG	VEQANWONFTLEGGVRVEKQKASIQYDKALIDRENYNHLPL				
a147	AVKQPMLLDNKVQHYSFFG	VEQANWONFTLEGGVRVEKQKASIRYDKALIDRENYNHLPL				
	430	440	450	460	470	480
m147.pep	460	470	480	490	500	510
	PDLGAHRQTARSFALS	GNWYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
a147	PDLGAHRQTARSFALS	GNWYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
	490	500	510	520	530	540
m147.pep	520	530	540	550	560	570
	HLNKERSNNIELALGYEG	DRWQYNLALYRNRFNGNYIYAQT	LNDRGRGPKSIEDDSEM	KLVR		
a147	HLNKERSNNIELALGYEG	DRWQYNLALYRNRFNGNYIYAQT	LNDRGRGPKSIEDDSEM	KLVR		

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	550	560	570	580	590	600
m147.pep	580	590	600	610	620	630
	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFFIAQDDQ					
a147	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFFIAQDDQ					
	610	620	630	640	650	660
m147.pep	640	650	660	670	680	690
	NAPRVPAARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
a147	NAPRVPAARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
	670	680	690	700	710	720
m147.pep	700	710	720	730		
	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
a147	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750	760		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

```

g148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGctgg  ttcaTCCCGA
51  AgctATgagt  gtcggcgCGC  TTGccgAcaa  AATCCGCAAA  AtcgaAAact
101 gGCCGCAAAA  AGgcaTCTTA  TTCCACGACA  TCACGCCCGT  CCTGCAAAGT
151 GCGGAATACT  TCCGCCTTTT  GGTGATTTG  CTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGCTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAG  CTCAaCGtcg  gctTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCCTATCG  CAAAGCTAcg  cgcTCGAATA
351 CGGGGAAGCT  GCGGTGGAAA  TCCACACCGa  tgccgTCAAA  CCCGTTTCGC
401 GCGTCCTGCT  GGTGATGAT  TTGGTTGCCA  CGGGCGGCAC  AATGCTTGCC
451 GGGCTGGAAC  TGATCCGCAA  ACTCGGCGGG  GAAATTGTCT  AAgccgcgcg
501 CATTTTGGAA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGCGCAAGTG
551 GCGCGCCCTT  ATTTACCCTG  CTTCAAAACG  AAGGCTGCAT  GAAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

```

g148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLQS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK
101 KGKLPFETVS  QSYALEYGEA  AVEIHTDAVK  PGSRVLLVDD  LVATGPTMLA
151 GLELIRKLGG  EIVEAAAILE  FTDLQGGKNI  RASGAPLFTL  LQNEGCMKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

```

m148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGCTGG  TTCATCCCGA
51  AGCTATGAGT  GTCGGCGCGC  TTGCCGACAA  AATCCGCAAA  ATCGAAAAC
101 GGCCGCAAAA  AGGCATCTTA  TTCCACGACA  TCACGCCCGT  CCTTCAAAGC
151 GCGGAATACT  TCCGCCTTTT  GGTGATTTA  TTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGTTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAG  CTCAACGTCG  GTTTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCCTATCG  CAAAGCTACG  CGCTCGAATA
351 CGGGGAAGCT  GCGGTGGAAA  TCCACACCGA  TGCCGTCAAA  CTCGGTTTCG
401 GCGTGCTGCT  GGTGATGAT  TTGATTGCCA  CGGGCGGCAC  GATGCTTGCC
451 GGAATGGAAC  TGATCCGCAA  ACTCGGCGGA  GAAATTGTCT  AAGCCGCCGC
501 CATTTTGGAA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGTGCAAGCG
551 GCGCGCCCTT  ATTTACCCTG  CTTCAAAACG  AAGGCTGTAT  GAAGGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

```

m148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLQS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK

```

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351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRLKGSWGVQ
401 YLGQKSSALS AIPETVQQPM LIDNNVRHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NQPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDRAWQYNLA AYRNRFNGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEII FYKPTPRYRIG VSGDYVRGRL KNLPSPGPRE DPYKRPFFIA
651 QADQNAIPRI AARLGPHLKT SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

m149-1.seq

```

1 ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51 CACACCCCCTC CTCGCCCAAG CGCATGAAAC TGAGCAATCG GTGGATTG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCGCCTC CGACAAAATC ATCTCCGGCG ATACCTTGCG
201 CCAAAAAGCC GTCAACTTGG GCGACGCTTT AGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGCGCTCTG CTCCCGTCAT TCGCGGTCAA
301 ACAGGCAGGC GGATTAAAGT GTTGAACCAT CACGGCGAAA CAGGCGATAT
351 GCGCGATTTT TCGCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTCGC
401 AACAGGTCGA AATCCTGCGC GGGCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTTGCCGAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAAC GCGGTATCGG GCGAACTCGG ATTGCGTTTG AGCAGCGGCA
551 ATCTGGAAAA ACTCACGTCC GCGCGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGCGTTAC CGCAATCTGA AACGCGTGCC CGACAGCCAC GCCGATTGCG
701 AAACGGGCGA CATCGGGCTG TCTTGGGTTG GCGAAAAAGG TTTTATCGGC
751 GTAGCGTACA GCGACCGTCG CGACCAATAT GGTCTGCCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGCTTGATTA
851 ACAAAACGTA TTTACAGCTT TATCCGCACC TGTTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATAATGC
951 ACACGCACAC ACCCACAGCG GCAGACCGTG GATAGACCTG CGCAACAAAC
1001 GCTACGAATC CCGTGCCGAA TGGAAGCAAC CGTTCCCGCG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCAGTC GAAAACCTTT TTAACAACCA AACGCAAAAC GCCCGCATCG
1151 AGTTGCCGCA CCAACCCATA GGTCGTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTTACAAC AAAAATCCAG TGCTTTATCT GCCATATCCG AAGCGGTTAA
1251 ACAACCGATG CTGCTTGACA ACAAAAGTGA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAATGGGAC AACTTCACGC TTGAAGGAGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGGA
1401 AAACCTACTA AACCAACCCC TGCCCGACCT CGGCGCGCAC CGCCAAACCG
1451 CCCGCTCATT CGCACTTTTC GGCACCTGGT ATTTACGCCC ACAACACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCCGTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAAAACAC TCGCCACCAA CACCTTGAA GTGCGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACGCA ACCGCTTCGG
1701 TAACTACATT TACGCCCCAA CCTTAAACGA CGGACGCGGC CCCAATCCAA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGCGGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTTCGGCGG ACTATGTACG AGGCGCTCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGAGAA GATGCCTACG GCAACCGTCC TTTTCATCGCA
1951 CAGGACGACC AAAATGCCCC CCGTGTTCCG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGTATCGA TGCCAATTTG GACTACTACC
2051 GCGTGTTGCG CCAAAACAAA CTCGCCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAAACTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAAT TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTTCTC TCTGATACG CGCAATGGG CCGCAGCTTT
2251 ACCGCGGCG TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

m149-1.pep

```

1 MAQTTLKPIV LSILLINTPL LAQAHETEQS VDLETVSVVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDT ALSQQVEILR GPVTLLYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSSELGLRL SSGNLEKLTS GGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTSGISL SWVGEKGFIF
251 VAYSRRRDQY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPLSCG FHDDDNAHAH THSGRPWIDL RNKRYELRAE WKQPPFGFEA
351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTQN ARIELRHQPI GRLKGSWGVQ
401 YLGQKSSALS AISEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIQYD KALIDRENY NHPLPDLGAH RQTARSFALS GNWYFTPQHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 601>:

1	ATGGCACAAA	TCACACTCAA	ACCCATTGTT	TTATCAATTC	TTTTAATCAA
51	CACACCCCTC	CTCGCCCAAG	CGCATGAAAC	TGAGCAATCG	GTGGGCTTGG
101	AAACGGCTAG	CGTCGTCCGC	AAAAGCCGTC	CGCGCGCGAC	TTCCGGGGCTG
151	CTGCACACTT	CGACCGCCTC	GCACAAAATC	ATCTCCGGCG	ATACTTTGCG
201	CCAAAAAGCG	GTCAACTTGG	GCGACGCTTT	GGACGGCGTA	CCGGGCATCC
251	ACGCTTCGCA	ATACGGCGCG	GGCGCATCCG	CTCCCGTTAT	TCGCGGTCAA
301	ACGGGCAGAC	GGATTAAGT	ATTGAACAT	CACGGCGAAA	CGGGCGATAT
351	GCGGGACTTT	TCTCCCGATC	ACGCCATTAT	GGTAGATACC	GCCTTGTGCG
401	AACAGGTTGA	AATCTTCGCC	GGGCGCGTTA	CGCTCTTGTA	CAGCTCGGGC
451	AATGTGGCGG	GGCTGGTGA	TGTTCCGAT	GAAAAAATCC	CGCAAAAAAT
501	GCCTGAAAAC	GGCGTATCGG	GCGAagccgG	ATTGCGTTTG	AGCAGCGGCA
551	ATTTAGAAAA	ACTGACATCC	GCAGGCATCA	ATATCGGACT	GGGCAAAAAAC
601	TTCGTGCTGC	ATACCGAAGC	CTTGATCCGC	AAATCGGGCG	ATTACGCCGT
651	ACCGCGTTAC	CGCAATCTGA	AGACCGCTGC	GCAGCGCAT	GCCGATTTCG
701	AAACGGGGCG	CATCGGGGTC	TCTTGGGTGG	GCGAAAAAGG	CTTTATCGGC
751	GCAGCATACA	CGCAGCGTCG	CGACCGCTAC	GGCCTGCCTG	CCCCAGGCCA
801	CGAATACGAT	GATTGCCACG	CGCATCATAT	TGGCGAAAAAG	AGTTTGATCA
851	ACAAACGCTA	TTTGCAGCTT	TATCCGCAT	TGTTGACCGA	AGAAGACATC
901	GATTACGACA	ATCCGGGCTT	GAGCTCGGCG	TTCACAGCAG	CGCAGCGGTG
951	ACACGCACAC	ACCCACAACG	GCAAAACGTG	GATAGACTCT	GCGCAACAAAC
1001	GCTACGAACT	CCGCGCCGAA	TGGAAGCAGC	CATTCCCCGG	TTTTGAAGCC
1051	CTGCGCGTAC	ATCTGAACCG	CAATGACTAC	CACCACGACG	AAAAAGCAGG
1101	CGATGCACTA	GAAACCTTCT	TACAACAACAA	AACACACAAAC	GCCCCGTATCG
1151	AGTTGCGCCA	CCAACCCATA	GGCCGTCTGA	AAGGCAGCTG	GGGCGTGCAC
1201	TATTTGGGAC	AAAAATCCAG	CGCGCTTTCC	GCCATTCCCC	AAACCGTCCA
1251	ACAACCGATG	TTGATTGACA	ACAATGTCCG	CGATTACAGC	TTTTTCGGTG
1301	TAGAACAGGC	AAATTGGGAC	AACCTTCACG	TTGAAGCGCG	CGTACGCGTG
1351	GAAAAACAAA	AAGCCTCCAT	CCGGTACGAC	AAAGCATTTA	TTGATTGAGA
1401	AAACTACTAC	AACCAAGCCC	TGCCGACCTT	CGGCGCGCAC	CGCCAAACCG
1451	CCCGCTCGTT	CGCACTTTCG	GGCAACTTGT	ATTTCAGCCG	ACACCAACAA
1501	CTCAGCCTCA	CGGCCTCCCA	TCAGGAACGC	CTGCCGTCAA	CGCAAGAACT
1551	GTACGCTACG	GGCAAGCAGC	TCGCCACCAA	CACCTTTTGA	GTGCGGCAAC
1601	AACACCTCAA	CAAGAGCGGT	TCCAACATA	TGCAACTCGC	GCTGGGCTAC
1651	GAAGGCGACC	GCTGGCAATA	CAATCTGGCA	GCCTACCGCA	ACCGATTTCG
1701	CAACTACATT	TACGCCCAAA	AGCTTAACGA	CGGACGCGCG	CCCAAAATCA
1751	TCGAAGACGA	CAGCGAAATG	AAGTCTGTGC	GCTACAAACC	ATCCGCTGCC
1801	GACTTCTACG	GCGCGGAAGG	CGAAATCTAC	TTCAAACCCG	ACCGCGCTA
1851	CCGCACTCGT	GTTTCCGGCG	ACTATTGACG	AGGCCGTCTG	AAAAACCTCG
1901	CGTCCCTACC	CGGCAAGGAA	GATCCCTACG	GCAAAACGTC	CTTCATCGCA
1951	CAAAGCGACC	AAAACGCCCC	CGCATTTCCG	GCTGCGCGCC	TCGGCTTCCA
2001	CCTGAAAAAC	TCGCTAACC	ACCGTATCGA	TGCCAAATTG	GACTACTACC
2051	CGGTGTTCGC	CCAAAACAAA	CTCGCCCGCT	ACGAAACGCG	TACGCGCGGA
2101	CACCATATGC	TCAACCTCGG	TGCAAACTAC	CGCCGCAATA	CGCGCTATGG
2151	CGAGTGAAT	TGGTACGTCA	AAGCGACAAA	CCTGCTCAAC	CAATCCGTTT
2201	ACGCCACAGC	CAGCTTCTCT	TCTGATACGC	CGCAAAATGG	CCGCGAGCTTT
2251	ACCGGCGGGC	TAAACGTGAA	GTTTTTAA		

This corresponds to the amino acid sequence <SEQ ID 602; ORF 149-1.ng>:

1	<u>MAQITLTKPIV</u>	<u>LSILLINTPL</u>	<u>LAQAHETEQS</u>	VGLETVSVVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQKA	VNLGDALDVG	PGIHASQYGG	GASAPVIRGQ
101	TGRRIKVLNH	HGETGDMADF	SPDHAIMVDV	ALSQQVEILR	GPVTLLYSSG
151	NVAGLVVDAD	GKIPKMPEN	GVSGEAGLRL	SSGNLEKITS	AGINIGLGKN
201	FVLHTEGLRY	KSGDYAVPRY	RNLKRLPDSH	ADSQTGSIGL	SWWGEKGFIG
251	AAYSDDRRDR	GLPHAHSHEYD	DCHADYIWOQ	SLINKRYLQL	YPHLLTEDDI
301	DYDNPLGSCG	FHDGDDGAHAH	THNGKPPWID	RNKRYELRAE	WKOPFPGEFA



551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA  
601 DFYGAEGEIIY FKPTPRYRIG VSGDYVRGRL KNLPSPGREG DAYGNRPPIA  
651 QDDQNAAPRVP AARLGFHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG  
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF  
751 TGGVNVKF\*

m149-1/g149-1 96.2% identity in 758 aa overlap

	10	20	30	40	50	60
m149-1.pep	MAQTTLKPIVLSILLINTPLLAQAHETE	QSV	DLET	VS	VVGKSRPRATS	GLLHTSTASDKI
g149-1	MAQITLKP	IVLSILLINTPLLAQAHETE	QSV	GLET	VS	VVGKSRPRATS
	10	20	30	40	50	60
	70	80	90	100	110	120
m149-1.pep	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF				
g149-1	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m149-1.pep	SPDHAIMVDTALSQQVEILRGPVTL	LYSSGNVAGLVDVADGKIPEKMPENGVS	GELGLRL			
g149-1	SPDHAIMVDTALSQQVEILRGPVTL	LYSSGNVAGLVDVADGKIPEKMPENGVS	GELGLRL			
	130	140	150	160	170	180
	190	200	210	220	230	240
m149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTE	GLYRKSGDYAVPRYRNLKRLPDSHADSQTGSIGL				
g149-1	SSGNLEKLTSGGINIGLGKNFVLHTE	GLYRKSGDYAVPRYRNLKRLPDSHADSQTGSIGL				
	190	200	210	220	230	240
	250	260	270	280	290	300
m149-1.pep	SWVGEKGFIVAYS	SDRRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHLLTEEDI			
g149-1	SWVGEKGFIVAYS	SDRRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHLLTEEDI			
	250	260	270	280	290	300
	310	320	330	340	350	360
m149-1.pep	DYDNPGLSCGFHDDDNAHAH	THSGRPWIDLRNKRYELRAEWKQPFPGFEALRVHLNRNDY				
g149-1	DYDNPGLSCGFHDDDNAHAH	THSGRPWIDLRNKRYELRAEWKQPFPGFEALRVHLNRNDY				
	310	320	330	340	350	360
	370	380	390	400	410	420
m149-1.pep	RHDEKAGDAVENFFNNQTQ	NARIELRHQPIGRLKGSWGVQYLQKSSALS	AISEAVKQPM			
g149-1	RHDEKAGDAVENFFNNQTQ	NARIELRHQPIGRLKGSWGVQYLQKSSALS	AISEAVKQPM			
	370	380	390	400	410	420
	430	440	450	460	470	480
m149-1.pep	LLDNKVQHYSFFGVEQANWDNFT	LEGGVRVEKQKASIYQDKALIDRENYNHPDLGAH				
g149-1	LLDNKVQHYSFFGVEQANWDNFT	LEGGVRVEKQKASIYQDKALIDRENYNHPDLGAH				
	430	440	450	460	470	480
	490	500	510	520	530	540
m149-1.pep	RQTARFALS	GNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER				
g149-1	RQTARFALS	GNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER				
	490	500	510	520	530	540
	550	560	570	580	590	600
m149-1.pep	SNNIELALGYEGDRWQYNLA	LYRNRFGNYIYAQTLNDGRGPKSIEDDSEM	KLVRYNQSGA			
g149-1	SNNIELALGYEGDRWQYNLA	LYRNRFGNYIYAQTLNDGRGPKSIEDDSEM	KLVRYNQSGA			
	550	560	570	580	590	600
	610	620	630	640	650	660
m149-1.pep	DFYGAEGEIIYFKPTPRYRIG	VSGDYVRGRLKNLPSPGREGDAYGNRPPIAQDDQNAAPRVP				
g149-1	DFYGAEGEIIYFKPTPRYRIG	VSGDYVRGRLKNLPSPGREDPYGKRPFIAQADQNAAPRIP				
	610	620	630	640	650	660

**a149-1.seq**

**a149-1.pep**

1	MAQTTLKPIV	LSILLINTPL	LSQAHGTEQS	VGLETVSVVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQKA	VNLGDALDGV	PGIHASQYGG	GASAPVIRSG
101	TGRRIKVLNH	HGETGDMADF	SPDHAMIVDS	ALSQQVEILR	GPVTLTRYSG
151	NVAGLVVDAD	GKIPKMPEN	GVSGELGLRL	SSGNLEKLTG	GGNIGLGNK
201	FVLHTEGLYR	KSGDYAVPRY	RNLKRLPDSH	ADSGTKISGL	SWGKEGTGFI
251	AAYSDDRRDQY	GLPAHSHEYD	DCHADIIWQK	SITNGRYLRL	YPHLLTEGDI
301	YDYNPGLSCG	FHDDDDAHAH	AHNGKPIWDL	RNRYELRAE	WQOPFPGFEA

351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVQ  
401 YLGQKSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV  
451 EKQKASIRYD KALIDRENY NHPPLDLGAH RQTARFALS GNWYFTPQHK  
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY  
551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA  
601 DFYGAEGEII FKPTPRYRIG VSGDYVRGRL KNLPSPGPRE DAYGNRPLIA  
651 QADQNAPRVP AARLGVHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG  
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF  
751 TGGVNVKF\*

a149-1/m149-1 98.0% identity in 758 aa overlap

a149-1.pep	MAQTTLKPIVLSILLINTPLLSQAHGTEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI
m149-1	MAQTTLKPIVLSILLINTPLLAQAHETEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI
a149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF
m149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF
a149-1.pep	SPDHAIMVDSALSQQVEILRGVPTLLYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL
m149-1	SPDHAIMVDTALSQQVEILRGVPTLLYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL
a149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL
m149-1	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL
a149-1.pep	SWVGEKGFIGAAYSDDRDQYGLPAHSHEYDDCHADI IWQKSLINKRYLQLYPHLLTEEDI
m149-1	SWVGEKGFIVAYSDDRDQYGLPAHSHEYDDCHADI IWQKSLINKRYLQLYPHLLTEEDI
a149-1.pep	DYDNPGLSGCFHDDDDAHAAHNGKPWIDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY
m149-1	DYDNPGLSGCFHDDDDNAHAHTSGRPWIDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY
a149-1.pep	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGVQYLGQKSSALSATSEAVKQPM
m149-1	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGVQYLGQKSSALSATSEAVKQPM
a149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPPLDLGAH
m149-1	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIYDKALIDRENYNHPPLDLGAH
a149-1.pep	RQTARFALS GNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER
m149-1	RQTARFALS GNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER
a149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM KLVRYNQSGA
m149-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM KLVRYNQSGA

a149-1.pep	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPLIAQADQNAPRVP
m149-1	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFIAQDDQNAPRVP
	610 620 630 640 650 660
a149-1.pep	AARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
m149-1	AARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
	670 680 690 700 710 720
a149-1.pep	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
m149-1	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
	730 740 750 759

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

g150.seq (partial)

```

1  ..TACTGCAAGG CAGACCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAT
51  CACCGCCCGC CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGTA
101 GCGGTTTCGA TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT
151 GACAACGATC CGGCACTGGT CGGGGAAATC CTAGACCTGC TCGGCATCAA
201 TCCGGCAACG GAAATACAGG CGGGCGGAAA AACCTGCGC GTTGCCTCCG
251 CACTGTTATC CCATTCGAA CTCACGAAA ACACCCCGC CTTGTCAAAA
301 GGCTATGCCA CGTTCGCCGA TAATGACGAA CTCGACCGTA TTGCTGCCGA
351 CAACGCCGTT TTGCAAGGCT TTGTGCAAAG CACGCCGATT GCCGGTGTGC
401 TGCACCGCTT CCCGGCAAAA CTGACGGCGG AACAATTCGC CGGCCTGCTG
451 CGCCCGCTTG CGCCGCGCCT GTATTGATT TCCTCGTCGC AGGCGGAAGC
501 GGGGGACGAA GTGCACCTGA CCGTCGGCGC AGTGCCTTTC GAACACGAAG
551 GGCAGCGCCG GCGGGCGGCG GCATCGGGTT TCTTTGCCGA CCGGCTGGAA
601 GAGGACGGCA CGGTGCGCGT GTTTGCGGAA CGCAACGACG GCTTCAGGCT
651 GCCCGAAGAC AGCCGCAAGC CGATTGTGAT GATCGGCTCC GGTACCGGCG
701 TCGCACCCTT CCGCGCCTTC GTCCAACAAC GTGCCGCGA AAATGCGGAA
751 GGCAGAAACT GGCTGATTTT CGGCAATCCG CATTTTGCCG CCGACTTCCT
801 CTATCAGACC GAATGCGAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT
851 ATGACTTCGC CTGGTCGCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC
901 AAAATCCGCG AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC
951 GCATATCTAT GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GAAGTGAAG
1001 CCGCCTTGCT GGATGTGATT ATCGGGGCG GGCATTGCGA CGAAGACGGC
1051 GCAGAAGGAT ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA
1101 TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

g150.pep (partial)

```

1  ..YCKADPFPA LLANQKITAR QSDKDVRHIE IDLSGSDLHY LPGDALGVWF
51  DNDPALVGEI LDLLGINPAT EIQAGGKTLV VASALLSHFE LTQNTPAFVK
101 GYATFADNDE LDRIAADNAV LQGFVQSTPI AGVLHRFPK LTAEQFAGLL
151 RPLAPRLYSI SSSQAEAGDE VHLTVGAVRF EHEGRARAGG ASGFFADRLE
201 EDGTVRVFAE RNDGFRLPED SRKPIVMIGS GTGVAPFRAF VQORAAENAE
251 GRNWLIFGNP HFAADFLYQT EWQQFAKDF LHRDYFAWSR DQEEKIYVQD
301 KIREQAEGLW QWLQEGAHYI VCGDAAKMAK EVEAALLDVI IGAGHSDEDE
351 AEGYLDMLRE EKRYQRDVY*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

m150.seq

```

1  ATGCAGAACA CAAATCCGCC ATTACCGCCT CTGCCGCCCG AAATCACGCA
51  GCTCCTGTCT GGGCTGGACG CGGCACAATG GGCGTGGCTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGAAAC GGGGCATCTG CAGGACTGCC CGCGCTTCAG
151 ACGGCATTGC CGCGCGCAGA ACCTTTTCC GTAACCGTCC TTTCCGCCTC
201 GCAAACCGGC AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251 AAGCCGCCCG CATCCAAGTC AGTCGCGCCG AACTGAAAGA CTATAAGGCG
301 AAAAACATCG CCGGCGAACG CCGCCTGCTG CTGGTTACCT CCACCCAAGG
351 CGAAGGCGAA CCGCGGAAAG AAGCCGTCGT GCTGCACAAA CTGCTGAACG
401 GCAAAAAAGC CCCGAAATTG GACAACTCC AATTGCGCGT ACTGGGTTTG

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